

BASE COUNT	78 a	PLC	I: Cloning sites, 5' end: <i>SakI</i> ; 3' end: <i>BamHI</i> ."
ORIGIN	31 c	36 g	
Query Match	4.7%	Score 19;	DB 29; Length 359;
Best Local Similarity	100.0%	Pred. No. 12;	
Matches	19;	Conservative	0;
Matches	0;	Mismatches	0;
Indels	0;	Gaps	0;
QY	99 aaaaaaaaaaaaaaaa	117	
Db	244 AAACCACTAGGAA	226	
QY	53 ctcattatccaaat	72	
Db	10 CCTCTATTTCAAAAT	28	
RESULT	2	PLC	I: Cloning sites, 5' end: <i>SakI</i> ; 3' end: <i>BamHI</i> ."
AL650451/c		EST	13-NOV-1997
LOCUS	AA650451	359 bp	mRNA
DEFINITION	ns98411.s1 NCI CGAP_Br4 Homo sapiens cDNA clone IMAGE:1191644		
ACCESSION			EST
VERSION	AA650451		
AA650451.1			GI:2577779
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
Bukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 359)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) This sequence version replaced 91:2286482.		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
CONVENT	TeI: (301) 496-1550		
EMAIL	Robert.Strausberg@nih.gov		
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.			
CDNA Library Preparation: David B. Kriman, Ph.D.			
CDNA Library Arrayed by: Greg Lennon, Ph.D.			
CDNA Sequencing by: Washington University Genome Sequencing Center			
Clone distribution by: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. consortium/LINL at: www-bio.lnl.gov/bbry/image.html			
Insert Length: 444 Std Error: 0.00			
Seq primer: 40m13 fwd. ER from Amersham.			
FEATURES	Location/Qualifiers		
source	1..359		
/organism="Homo sapiens"			
/db_xref="taxon:9605"			
/clone="IMAGE:1191644"			
/clone_id="NCI_CGAP_Br4"			
/sex="Female"			
/tissue_type="normal ductal tissue"			
/lab_host="DH10B"			
/note="Organ: breast; Vector: pAMP10; mRNA made from normal breast ductal tissue; cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Kriman et al. (1996) Cancer Research 56:5380-5383."			
BASE COUNT	82 a	108 c	101 g
ORIGIN	81 t	5 others	
Query Match	4.7%	Score 19;	DB 94; Length 377;
Best Local Similarity	100.0%	Pred. No. 12;	
Matches	19;	Conservative	0;
Matches	0;	Mismatches	0;
Indels	0;	Gaps	0;
QY	36 ttcaagttctcggtgttcc	54	
Db	9 TTTCAGCTTCCTGGGTTC	27	
RESULT	4	PLC	I: Cloning sites, 5' end: <i>SakI</i> ; 3' end: <i>BamHI</i> ."
AQ52552		EST	24-JAN-1999
LOCUS	AQ352552	470 bp	DN
DEFINITION	CITB-EL-254101.TF CITB-EL Homo sapiens genomic clone 254101, genomic survey sequence.		
ACCESSION	AQ352552		
VERSION	AQ352552.1		
KEYWORDS	GSS.		
SOURCE	Homo sapiens		
ORGANISM	Bukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 470)		
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.		
TITLE	Use of BAC End sequences from Caltech Libraries for Sequence-Ready Map Building		

Db 11526 AAACTTAAGTGTAA 11541

RESULT 31 AC034173/c DEFINITION Homo sapiens chromosome 11 clone RP11-689019, WORKING DRAFT

SEQUENCE: 17 ordered pieces.

ACCESSION AC034173

VERSION AC034173.2

KEYWORDS HTGS; HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 172191)

AUTHORS Waterston, R.H.

TITLE Waterston, R.H.

JOURNAL Submitted (04-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Apr 16, 2000 this sequence version replaced 91:7408159.

Center: Washington University Genome Sequencing Center

Center project: Project Information

Center project: Summary Statistics

Sequencing vector: M13; 100%

Sequencing vector: plasmid; 0%

Chemistry: Dye-primer; M13: 100% of reads

Chemistry: Dye-terminator; Big Dye; 0% of reads

Assembly program: Phrap; version: 0.90319

Consensus quality: 16684 bases at least 0.0

Consensus quality: 16875 bases at least 0.0

Consensus quality: 15947 bases at least 0.20

Insert size: 18100; agarose-fp

Insert size: 17059; sum-of-contigs

Quality coverage: 4.63 in Q20 bases; agarose-fp

Quality coverage: 4.94 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 2132: contig of 2932 bp in length

2133 4962: contig of 2730 bp in length

4963 5062: gap of unknown length

5063 8009: contig of 2947 bp in length

8010 8109: gap of unknown length

8110 11516: contig of 3047 bp in length

11517 11526: gap of unknown length

11617 18870: contig of 5254 bp in length

16871 16970: gap of unknown length

16971 21936: contig of 4966 bp in length

21937 22036: gap of unknown length

22037 26484: contig of 4448 bp in length

2223 26584: gap of unknown length

26585 34255: contig of 7670 bp in length

34354: gap of unknown length

34355 42316: contig of 7962 bp in length

42417 42417: gap of unknown length

51658: contig of 9242 bp in length

RESULT 32 HUM22DC982 DEFINITION Homo sapiens (subclone 4_c6 from P1 H22) DNA sequence.

LOCUS HUM22DC982 2573 bp DNA PRI 01-SEP-1995

VERSION L46904

KEYWORDS L46904.1 GR:972739

ORGANISM Homo sapiens (tissue library: Subclones in por2 from P1 clone H22)

Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2737)

AUTHORS Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A., Ericsson,C.L., Jukliev,M.A., Kim,R.J., Lee,M.T., Li,M., Mayeda,C.A., Steerle-El Kheir,A. and Palizzolo,M.J.

TITLE Sequencing of the interleukin gene cluster of homo sapiens

JOURNAL Unpublished (1995)

COMMENT This subclone overlaps H22_8_c11 and H22_5_c7. The P1, from which this subclone is derived, is adjacent to P1. Sequence submitted by: Human Genome Center

Lawrence Berkeley Laboratory

Berkeley, CA 94720

e-mail: seqgenome.lbl.gov.

FEATURES source

1. 2573

/organism="Homo sapiens"

/db_xref="taxon:9006"

BASE COUNT 1000 a 452 c 531 g 590 t

Query Match Similarity 40.8%; score 75; DB 10; Length 2573;

Best Local Similarity 100.0%; Pred. No. 6.1e-29;

